Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:28:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094029.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_ERR2094029 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094029_1.fastq.gz ERR2094029_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:28:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR2094029.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	432,574
Mapped reads	402,472 / 93.04%
Unmapped reads	30,102 / 6.96%
Mapped paired reads	402,472 / 93.04%
Mapped reads, first in pair	202,344 / 46.78%
Mapped reads, second in pair	200,128 / 46.26%
Mapped reads, both in pair	396,912 / 91.76%
Mapped reads, singletons	5,560 / 1.29%
Secondary alignments	0
Supplementary alignments	21,721 / 5.02%
Read min/max/mean length	30 / 151 / 142.63
Duplicated reads (estimated)	373,079 / 86.25%
Duplication rate	44.61%
Clipped reads	194,330 / 44.92%

2.2. ACGT Content

Number/percentage of A's	14,387,650 / 28.03%
Number/percentage of C's	11,269,690 / 21.96%
Number/percentage of T's	13,850,376 / 26.98%
Number/percentage of G's	11,821,793 / 23.03%
Number/percentage of N's	606 / 0%

GC Percentage	44.99%

2.3. Coverage

Mean	0.0169
Standard Deviation	5.5724

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Insert size

Mean	485,335.12
Standard Deviation	6,366,896.39
P25/Median/P75	136 / 171 / 210

2.6. Mismatches and indels

General error rate	3.72%
Mismatches	1,839,461
Insertions	33,260
Mapped reads with at least one insertion	8.1%
Deletions	130,937
Mapped reads with at least one deletion	31.32%
Homopolymer indels	27.71%

2.7. Chromosome stats

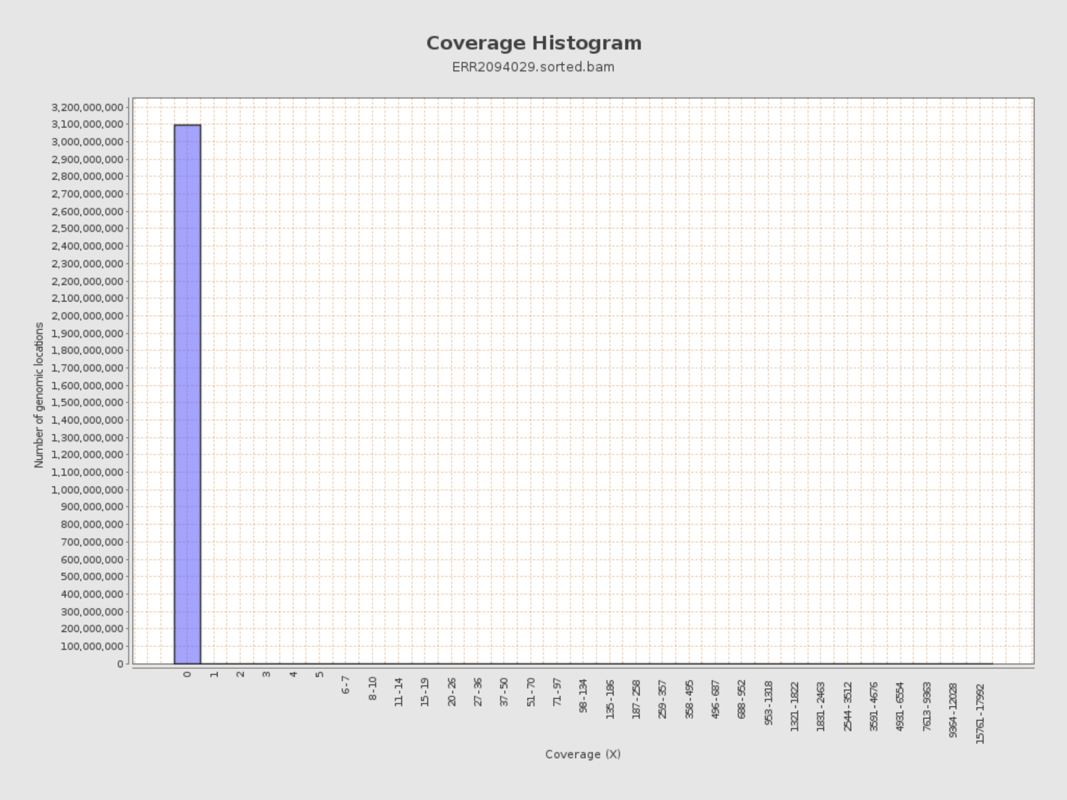
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	824969	0.0033	0.9824
chr2	243199373	2622376	0.0108	2.522
chr3	198022430	897339	0.0045	1.329
chr4	191154276	604287	0.0032	0.6528
chr5	180915260	923445	0.0051	1.5917
chr6	171115067	1725844	0.0101	4.5496
chr7	159138663	1391719	0.0087	2.3506
chr8	146364022	1074774	0.0073	2.2847
chr9	141213431	763931	0.0054	1.9053
chr10	135534747	975418	0.0072	1.6871
chr11	135006516	1384054	0.0103	2.3061
chr12	133851895	2259510	0.0169	5.0167
chr13	115169878	719403	0.0062	1.8889
chr14	107349540	525277	0.0049	1.05
chr15	102531392	543845	0.0053	1.3146
chr16	90354753	386626	0.0043	1.0119
chr17	81195210	1610842	0.0198	4.3606
chr18	78077248	196163	0.0025	0.5524
chr19	59128983	371238	0.0063	0.9145
chr20	63025520	552472	0.0088	3.0631
chr21	48129895	180137	0.0037	0.5876
chr22	51304566	166226	0.0032	0.431
chrMT	16571	7440796	449.0252	1,934.7958
chrX	155270560	23856642	0.1536	9.7682

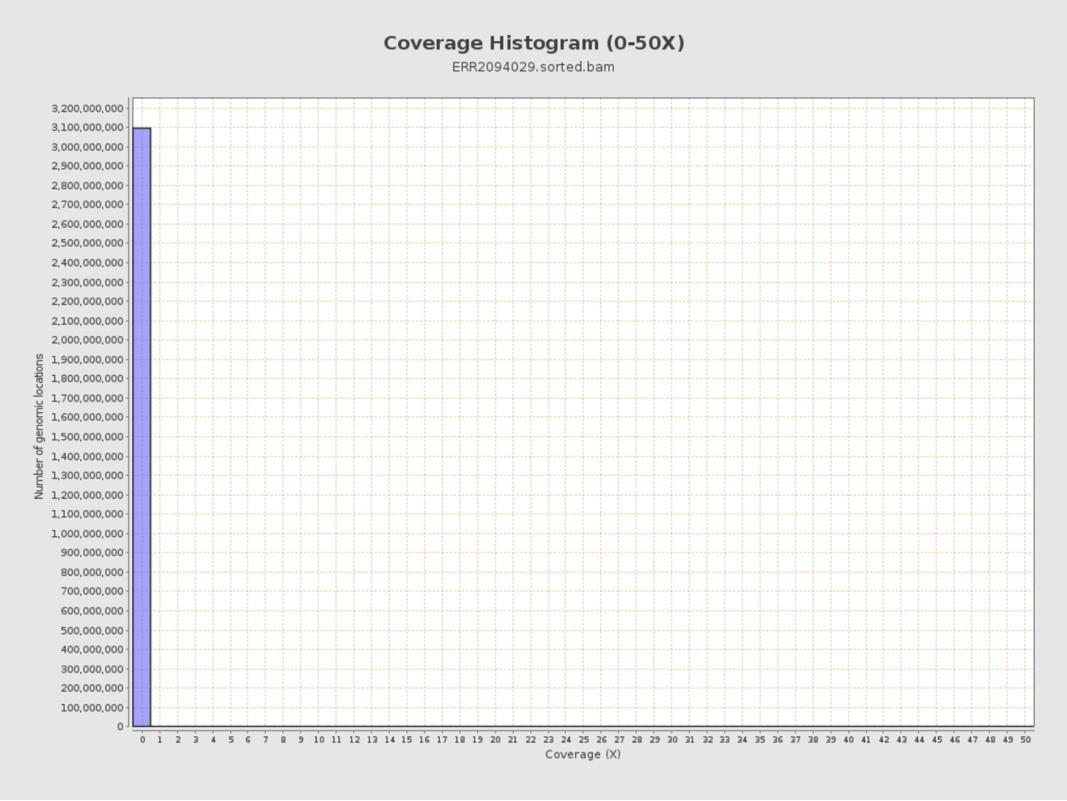
chrY	59373566	390779	0.0066	1.0318

3. Results : Coverage across reference

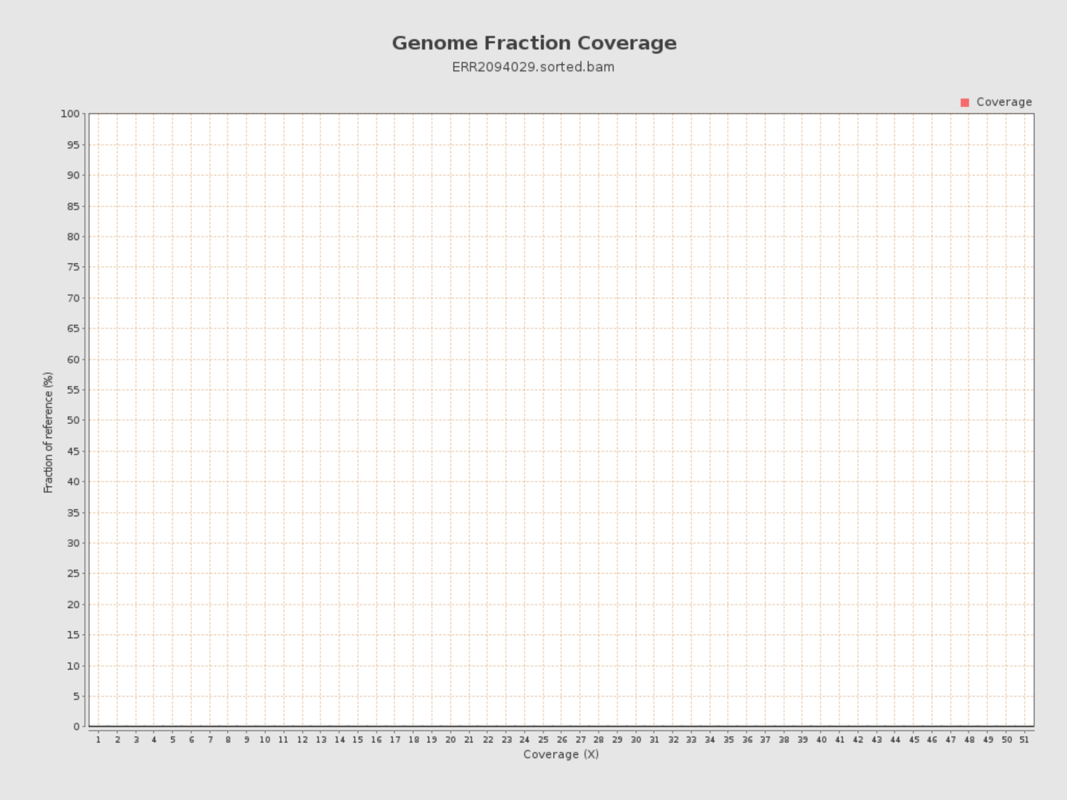
4. Results : Coverage Histogram



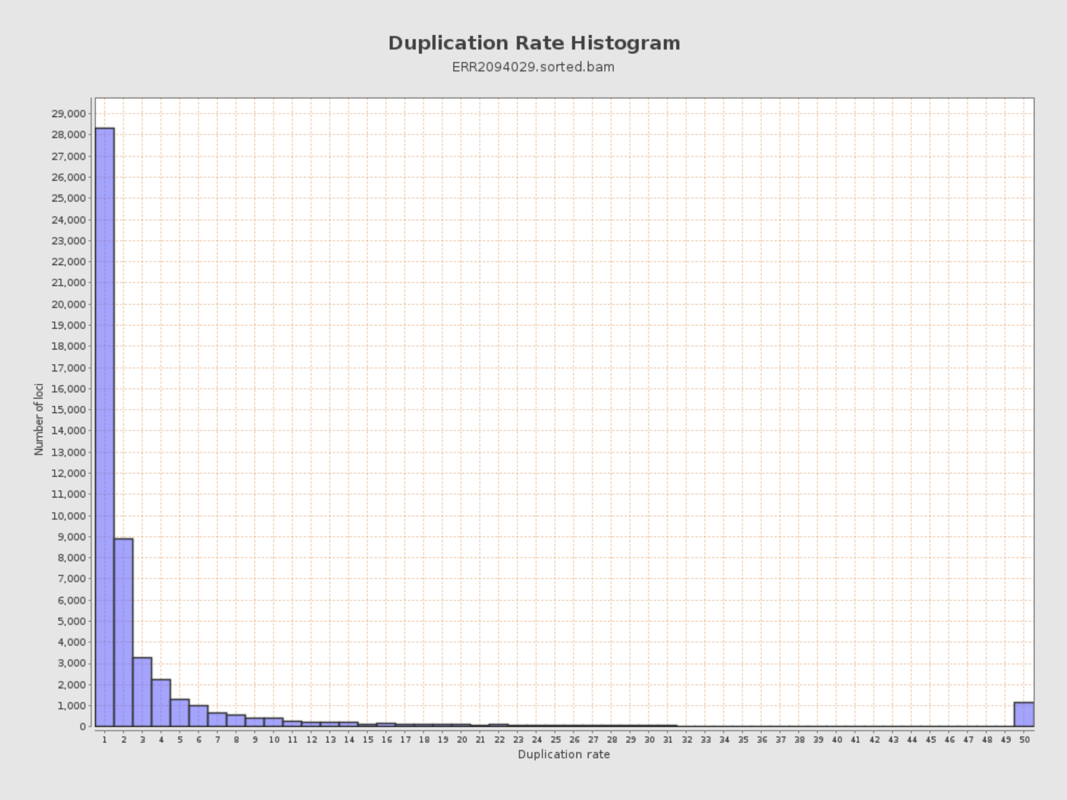
5. Results : Coverage Histogram (0-50X)



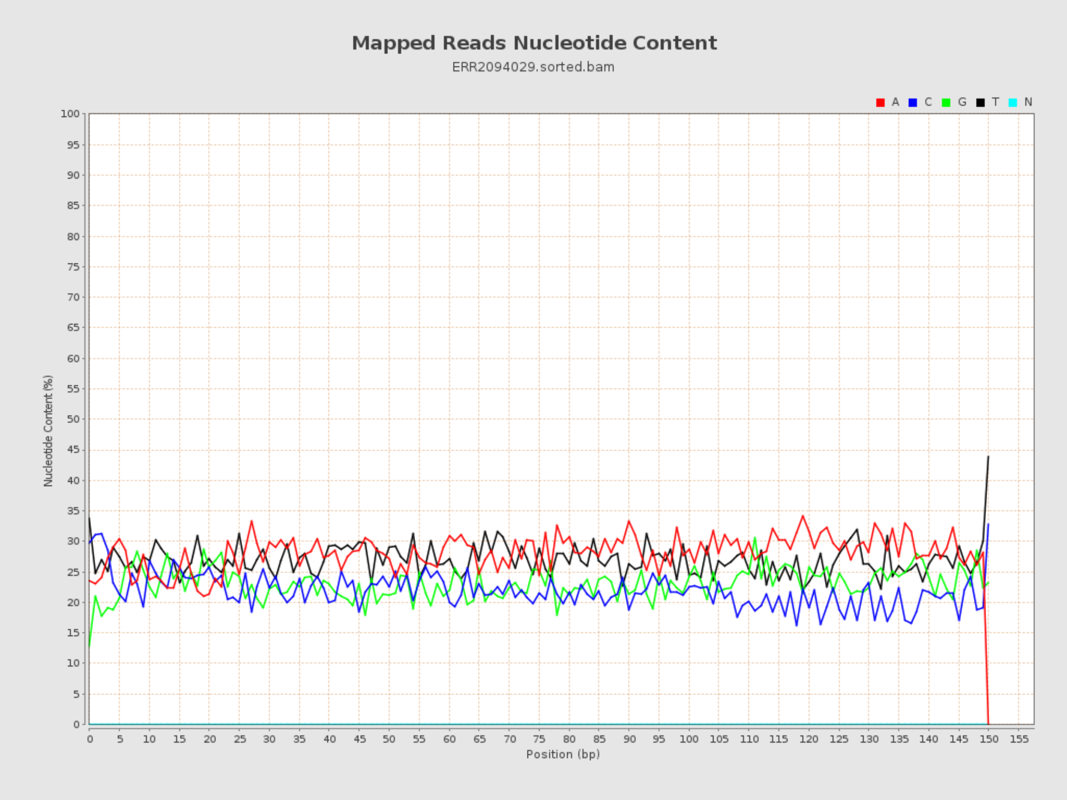
6. Results : Genome Fraction Coverage



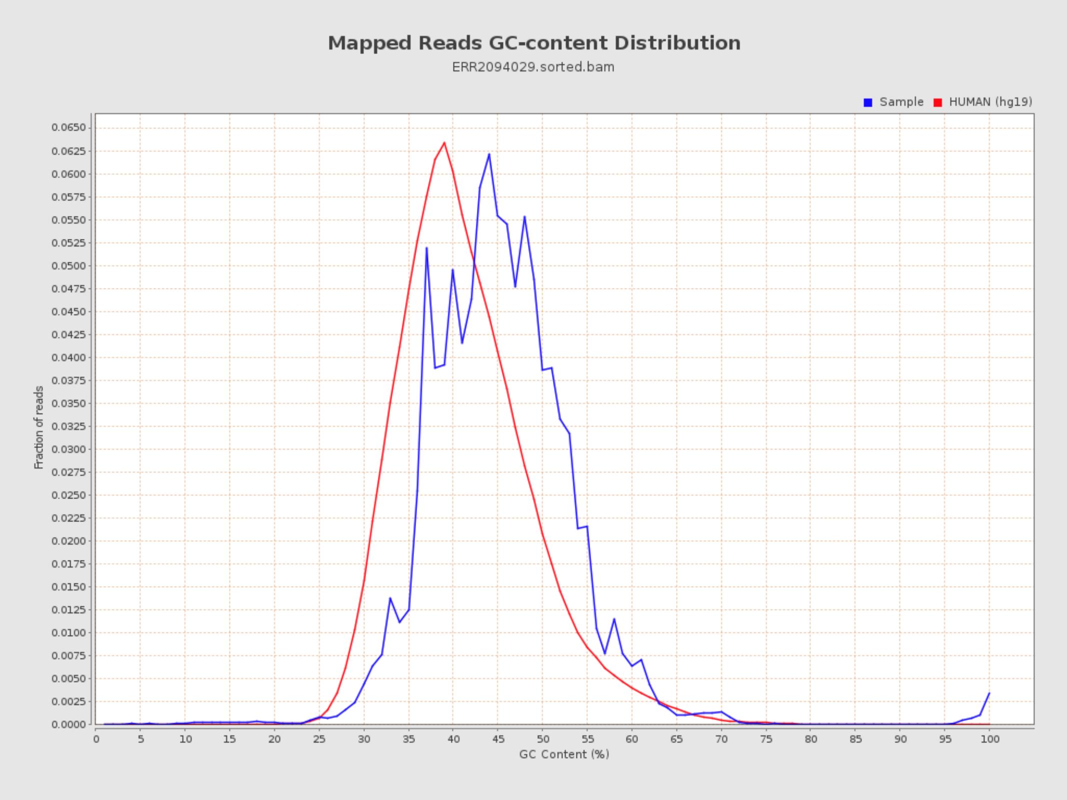
7. Results : Duplication Rate Histogram



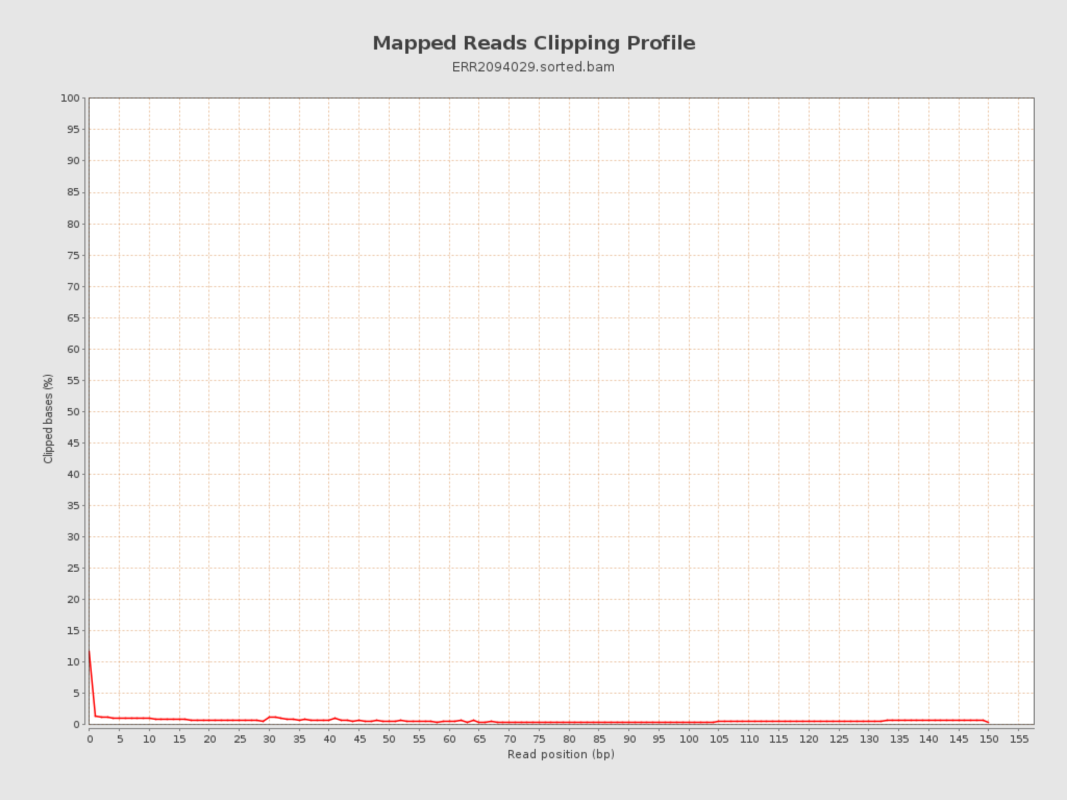
8. Results : Mapped Reads Nucleotide Content



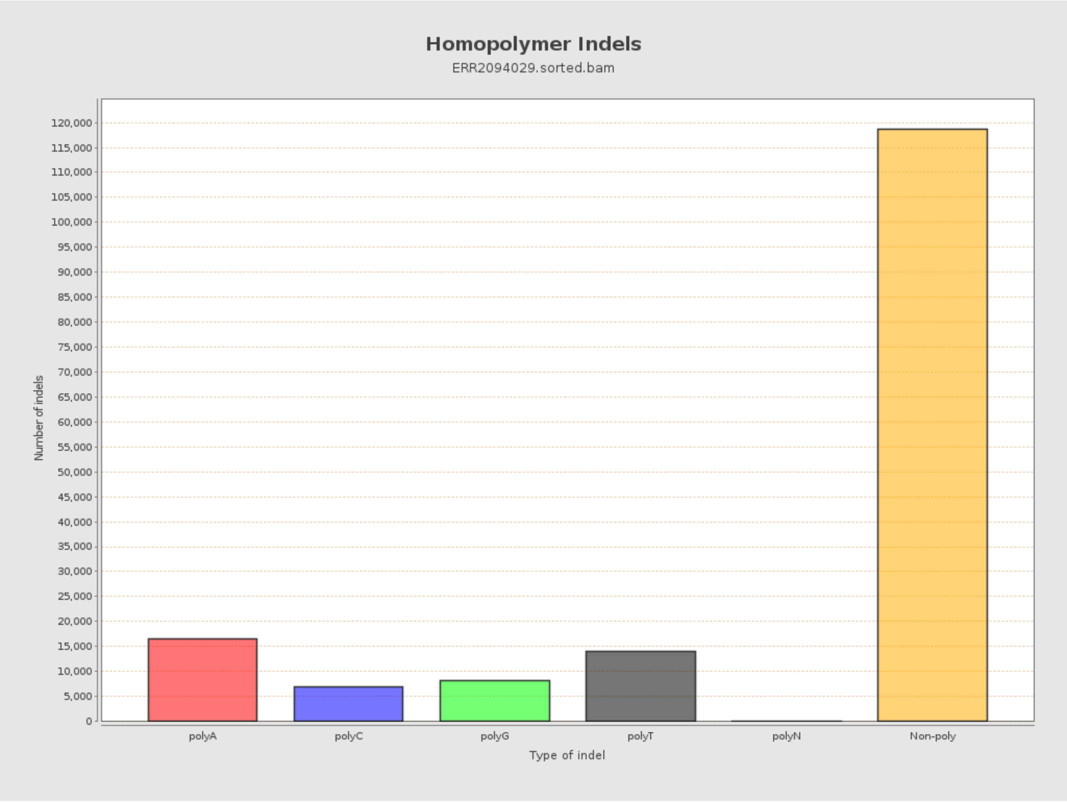
9. Results : Mapped Reads GC-content Distribution



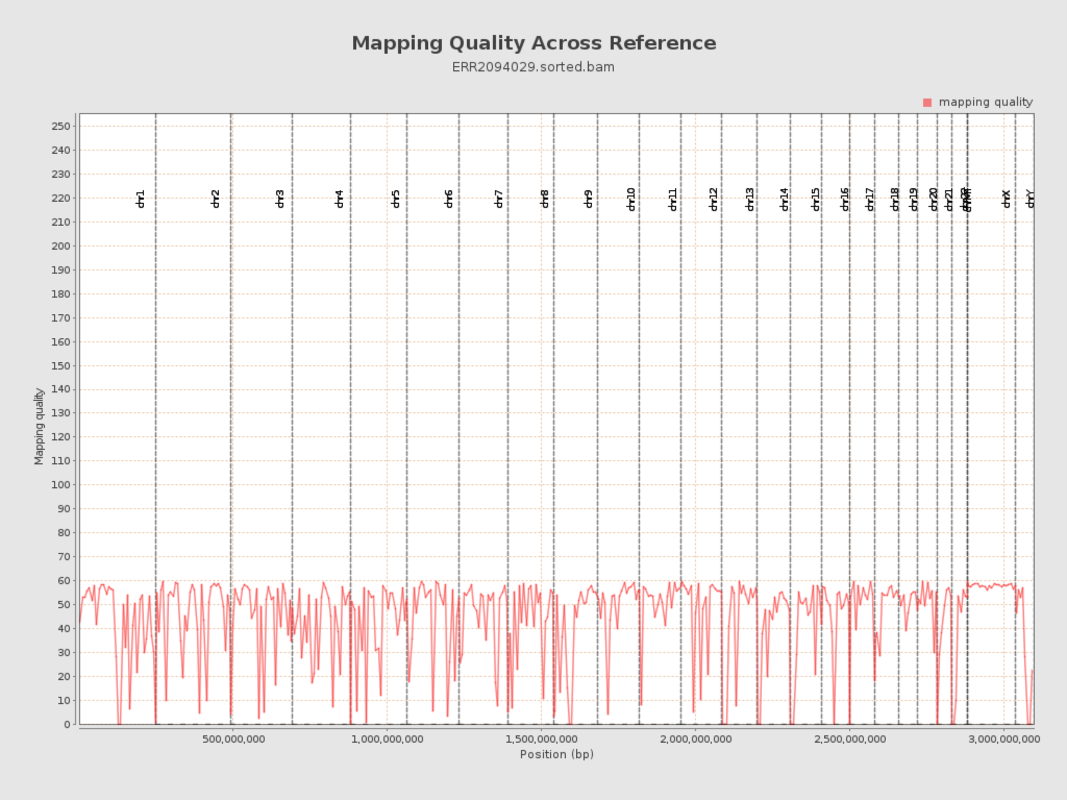
10. Results : Mapped Reads Clipping Profile



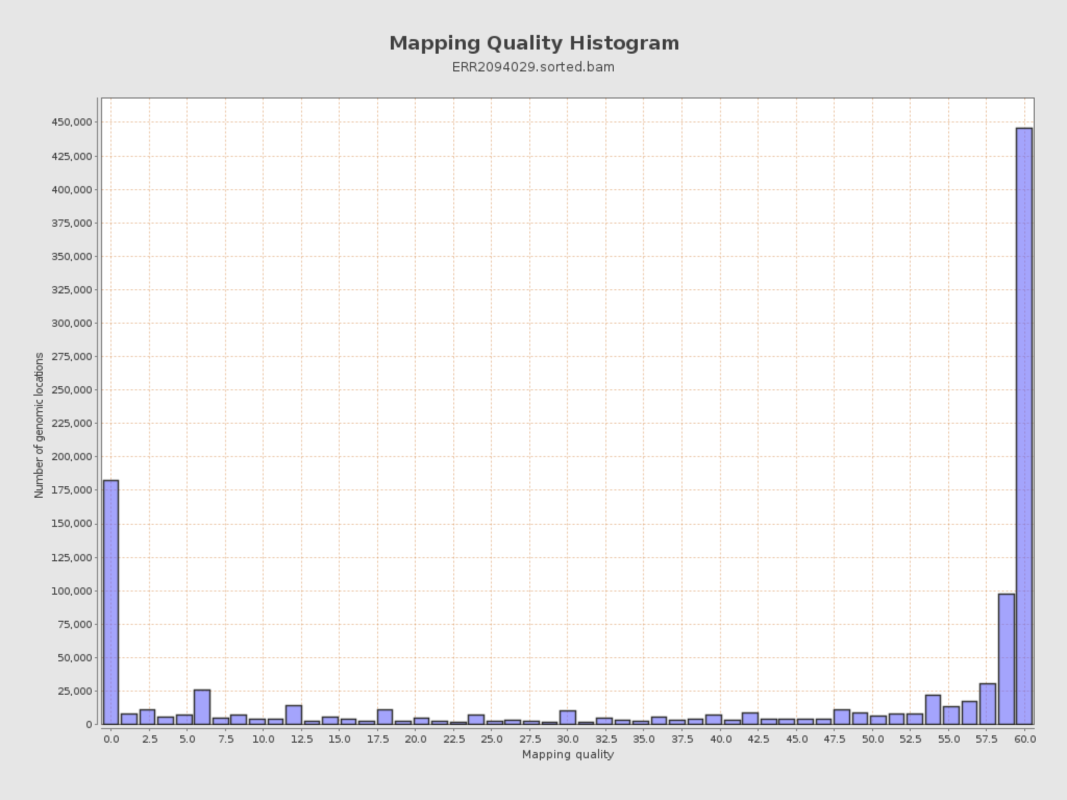
11. Results : Homopolymer Indels



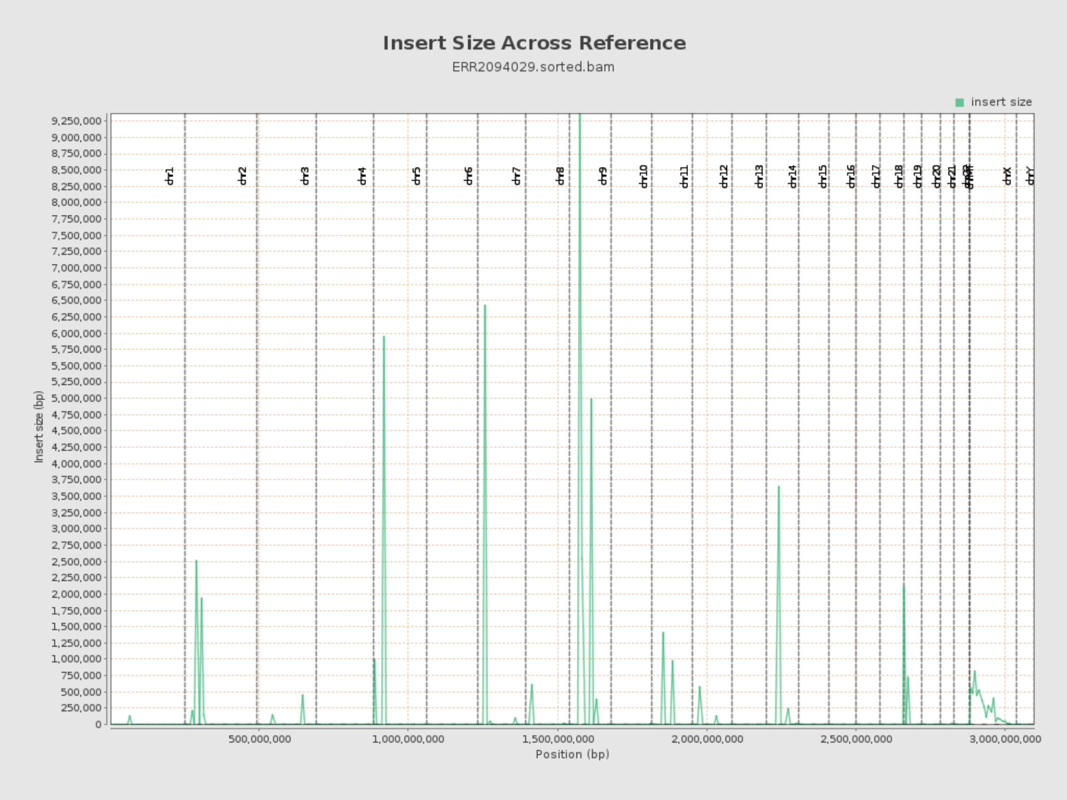
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram